PCT/AU99/00691 09.04.2000

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                                        ctagccaccacttgtcttcacggtg      116

ATGTTGGACTCCGTAACCCATAGCACCTTCCTGCCCAACGCATCCTTCTGTGACCCCCTG      176

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GAATGGCTCCAATTCTGCTGTGACCAGTACAAGCTTGATGCCAACTGCATCTCCTTCTGT      356

CACTTCAACATCAGCGGCCTGCAGCTCTGCAGCATGACGCAGGAGGAGTTCATTGAGGCA      416

GCCGGCATCTGTGGGGAGTACCTGTACTTCATTCTCCAGAACATTCGCTCGCAAGGTTAC      476

TCCTTTTTCAATGATGCTGAAGAGACCAAGACTGGCATCAAAGACTATGCTGATTCCAGT      536

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CTGGAATGGGAAGACAGGGAGCAGGGCATTTTCCGAGTGGTTAAGTCAGAAGCCCTGGCA      716

AAGATGTGGGGACAAAGGAAGAAGAATGACAGGATGACGTACGAGAAGCTGAGCCGAGCC      776

CTGAGATACTACTATAAAACGAGAATTCTGGAGCGGGTTGACCGGAGGTTAGTGTACAAA      836

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Figure 1a

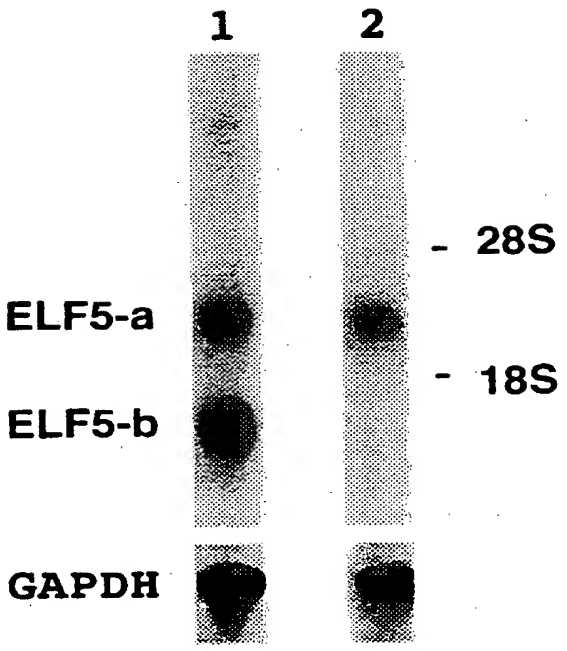

Figure 1b

TOET80"Eh098760

SUBSTITUTE SHEET (Rule 26) (RO/AU)

09/786043

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mELF5   MLDSVTHSTFLPNASFCDPLMPWTDLFSNEDYYPAFEHQTACDSYWTSVH   50
                      CKII          CKII          CKII

hELF5   PEYWTKRHVWEWLQFCCDQYKLDTNCISFCNFNISGLQLCSMTQEEFVEA   100
mELF5   PEYWTKRHVWEWLQFCCDQYKLDANCISFCHFNISGLQLCSMTQEEFIEA   100
          PKC                                     CKII

hELF5   AGFCGEYLYFILQNIRTQGYSFFNDAEESKATIKDYADSNCLKTSGIKSQ   150
mELF5   AGICGEYLYFILQNIRSQGYSFFNDAEETKTGIKDYADSSCLKTSGIKSQ   150

hELF5   DCHSHSRTSLQSSHLWEFVRDLLLSPEENCGILEWEDREQGIFRVVKSEA   200
mELF5   DCHS--RTSLQSSHLWEFVRDLLLSPEENCGILEWEDREQGIFRVVKSEA   198
                                  CKII

hELF5   LAKMWGQRKKNDRMTYEKLSRALRYYYKTGILERVDRRLVYKFGKNAHGW   250
mELF5   LAKMWGQRKKNDRMTYEKLSRALRYYYKTRILERVDRRLVYKFGKNAHGW   248
                      TyP

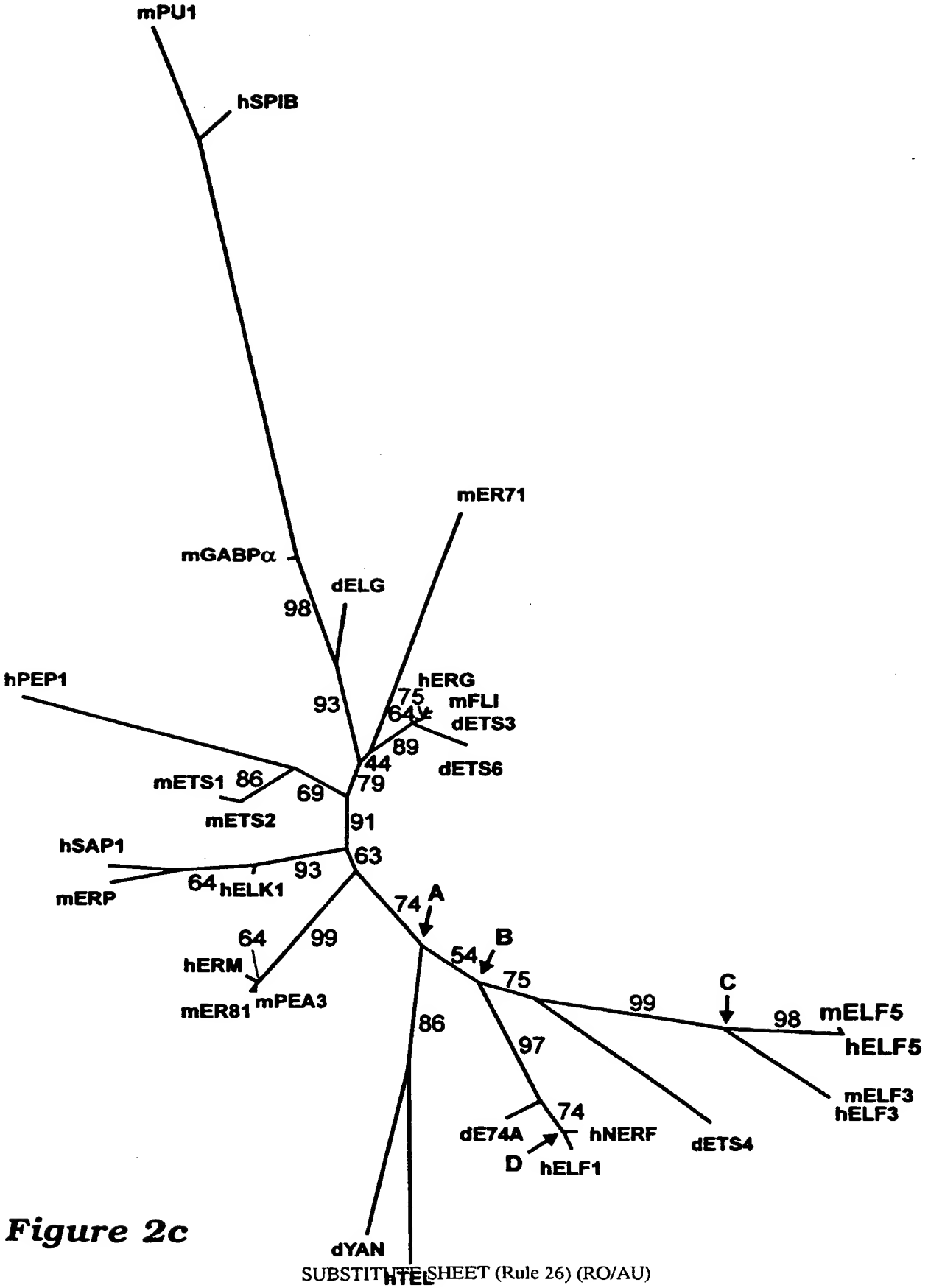
hELF5   QEDKL*                                              255
mELF5   QEEKL*                                              253
```

Figure 2a

		IDENTITY (%)
hELF5	LWEFVRDLLLSPE-ENCGILEWEDREQGIFRVV--KSEALAKMWGQRK-KNDRMTYEKLSRALRYYYKTGILERVD--RRLVYKF	100
mELF5	LWEFVRDLLLSPE-ENCGILEWEDREQGIFRVV--KSEALAKMWGQRK-KNDRMTYEKLSRALRYYYKTRILERVD--RRLVYKF	98
hELF3	LWEFIRDILIHPE-LNEGLMKWENRHEGVFKFL--RSEAVAQLWGQKK-KNSNMTYEKLSRAMRYYYKREILERVD-GRRLVYKF	67
mELF3	LWEFIRDILIHPE-LNEGLMKWENRHEGVFKFL--RSEAVAQLWGQKK-KNSNMTYEKLSRAMRYYYKREILERVD-GRRLVYKF	67
hNERF	LWEFLLDLLQDKN-TCPRYIKWTQREKGIFKLV--DSKAVSKLWGKHK-NKPDMNYETMGRALRYYYQRGILAKVE-GQRLVYQF	49
dETS4	LWQFLKELLASPQ-VNGTAIRWIDRSKGIFKIE--DSVRVAKLWGRRK-NRPAMNYDKLSRSIRQYYKKGIMKKTERSQRLVYQF	48
dE74A	LWEFLLKLLQDRE-YCPRFIKWTNREKGVFKLV--DSKAVSRLWGMHK-NKPDMNYETMGRALRYYYQRGILAKVD-GQRLVYHF	48
hELF1	LWEFLLALLQDKA-TCPKYIKWTQREKGIFKLV--DSKAVSRLWGKHK-NKPDMNYETMGRALRYYYQRGILAKVE-GQRLVYQF	46
hELK1	LWQFLLQLLREQ--GNGHIISWTSRDGGEFKLV--DAEEVARLWGLRK-NKTNMNYDKLSRALRYYYDKNIIRKVS-GQKFVYKF	46
hTEL	LWDYVYQLLSDS--RYENFIRWEDKESKIFRIV--DPNGLARLWGNHK-NRTNMTYEKMSRALRHYYKLNIIRKEP-GQRLLFRF	44
hERM	LWQFLVTLLDDP--ANAHFIAWTGR-GMEFKLI--EPEEVARRWGIQK-NRPAMNYDKLSRSLRYYYEKGIMQKVA-GERYVYKF	44
mER81	LWQFLVALLDDP--SNSHFIAWTGR-GMEFKLI--EPEEVARRWGIQK-NRPAMNYDKLSRSLRYYYEKGIMQKVA-GERYVYKF	44
mPEA3	LWQFLVALLDDP--TNAHFIAWTGR-GMEFKLI--EPEEVARLWGIQK-NRPAMNYDKLSRSLRYYYEKGIMQKVA-GERYVYKF	44
mGABPα	LWQFLLELLTDK--DARDCISWVGDEG-EFKLN--QPELVAQKWGQRK-NKPTMNYEKLSRALRYYYDGDMICKVQ-GKRFVYKF	44
mERP	LWQFLLHLLLDQ--KHEHLICWTSNDG-EFKLL--KAEEVAKLWGLRK-NKTNMNYDKLSRALRYYYDKNIIKKVI-GQKFVYKF	42
dETS6	LWQFLLELLADS--SNANAISWEGQSG-EFRLI--DPDEVARRWGERK-AKPNMNYDKLSRALRYYYDKNIMTKVH-GKRYAYKF	42
mPU1	LYQFLLDLLRSG--DMKDSIWWVDKDKGTFQFSSKHKEALAHRWGIQKGNRKKMTYQKMARALRNYGKTGEVKKVK--KKLTYQF	42
hPE1	LWHFILELLQKE--EFRHVIAWQQGEYGEFVIK--DPDEVARLWGRRK-CKPQMNYDKLSRALRYYYNKRILHKTK-GKRFTYKF	42
hSAP1	LWQFLLQLLQKP--QNKHMICWTSNDG-QFKLL--QAEEVARLWGIRK-NKPNMNYDKLSRALRYYYVKNIIKKVN-GQKFVYKF	42
hSPIB	LYQFLLGLLTRG--DMRECVWWVEPGAGVFQFSSKHKELLARRWGQQKGNRKRMTYQKLARALRNYAKTGEIRKVK--RKLTYQF	42
dYAN	LWDFLQQLLNDRNQKYSDLIAWKCRDTGVFKIV--DPAGLAKLWGIQK-NHLSMNYDKMSRALRYYYRVNILRKVQ-GERHCYQF	41
hERG	LWQFLLELLSDS--SNSSCITWEGTNG-EFKMT--DPDEVARRWGERK-SKPNMNYDKLSRALRYYYDKNIMTKVH-GKRYAYKF	41
mFLI1	LWQFLLELLSDS--ANASCITWEGTNG-EFKMT--DPDEVARRWGERK-SKPNMNYDKLSRALRYYYDKNIMTKVH-GKRYAYKF	41
dELG	LWQFLLEILTDC--EHTDVIEWVGTEG-EFKLT--DPDRVARLWGEKK-NKPAMNYEKLSRALRYYYDGDMISKVS-GKRFAYKF	40
dETS3	LWQFLLELLSDS--NNASCITWEGTNG-EFKLT--DPDEVARRWGERK-SKPNMNYDKLSRALR----------	39
mETS1	LWQFLLELLTDK--SCQSFISWTGDGW-EFKLS--DPDEVARRWGKRK-NKPKMNYEKLSRGLRYYYDKNIIHKTA-GKRYVYRF	37
mETS2	LWQFLLELLSDK--SCQSFISWTGDGW-EFKLA--DPDEVARRWGKRK-NKPKMNYEKLSRGLRYYYDKNIIHKTS-GKRYVYRF	37
mER71	LWQFLLKLLQDG--ARSSCIRWTGNSR-EFQLC--DPKEVARLWGERK-RKPGMNYEKLSRGLRYYYRRDIVLKSG-GRKYTYRF	36
consensus	LWQFLL LL D I W FK VAR WG K P MNY KLSR LRYYY I K GR Y F	

Figure 2b

T02T80 "Eh0980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89
44
dETS6
mETS1
86
69
79
mETS2
91
hSAP1
63
64
hELK1
93
mERP
74
A
64
99
B
hERM
54
75
C
99
98
mELF5
hELF5
mER81
mPEA3
86
97
mELF3
hELF3
74
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D
hELF1
dYAN
hTEL

Figure 2c

FOSTER "Ethics"

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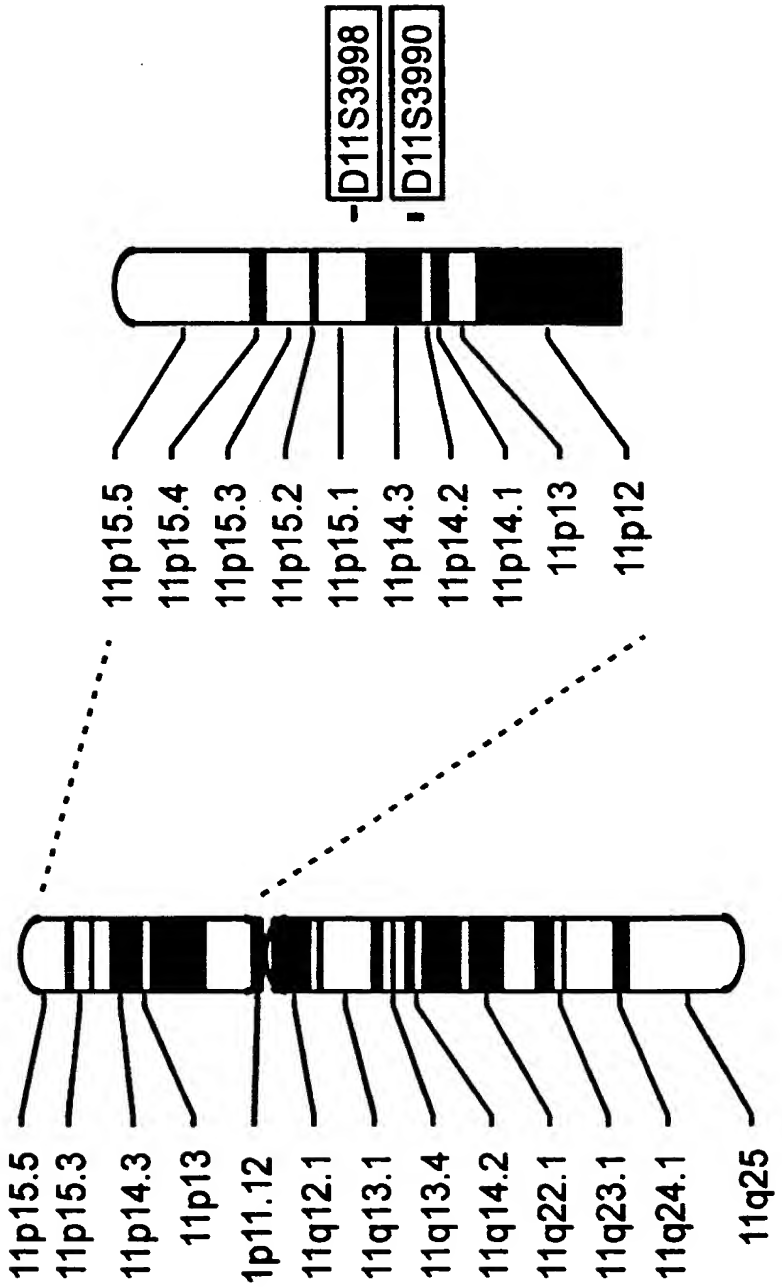
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D11S3990
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11p15.4
11p15.3
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11p12
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11p13
11p11.12
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11q25

Figure 3

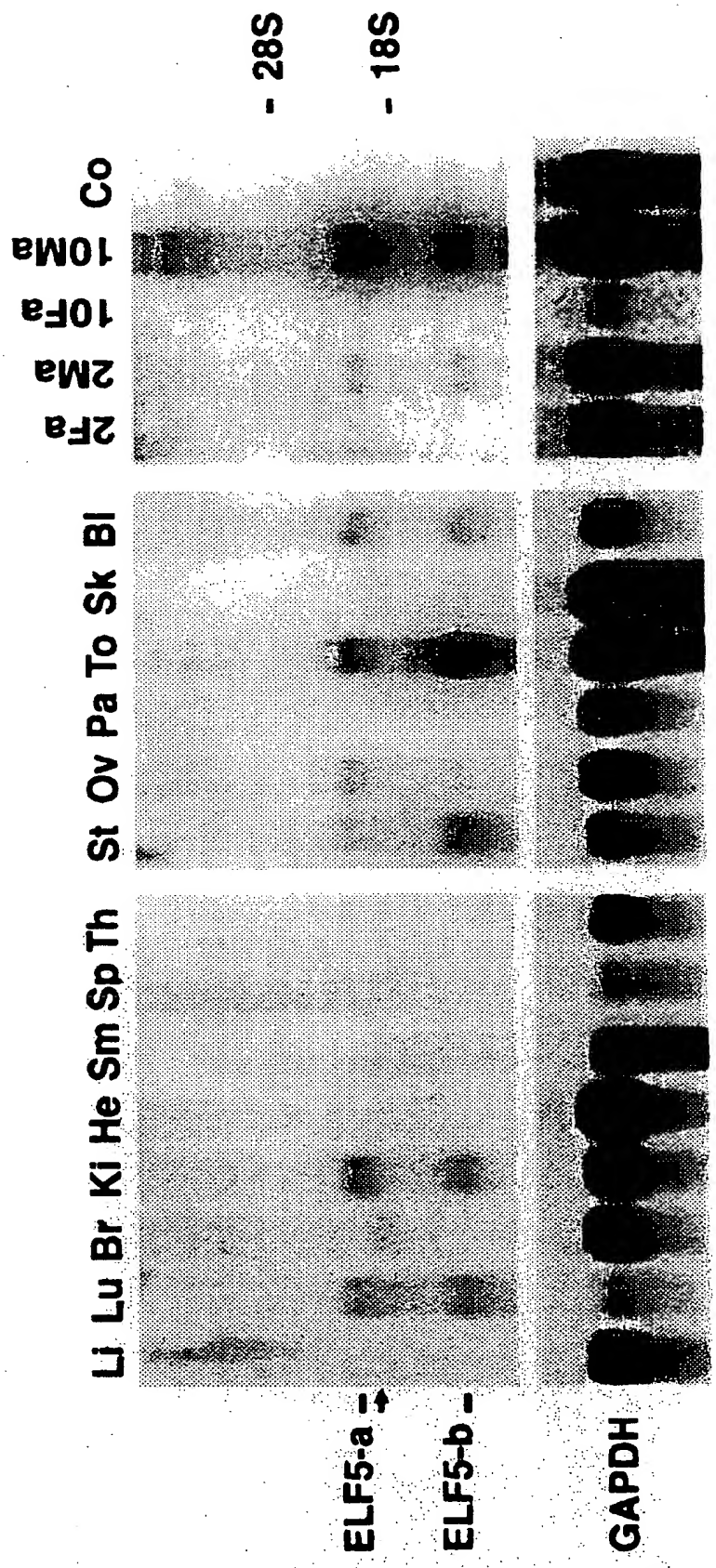

- 28S
- 18S
Co
10Ma
10Fa
2Ma
2Fa
St Ov Pa To Sk Bl
Li Lu Br Ki He Sm Sp Th
ELF5-a
ELF5-b
GAPDH

Figure 4a

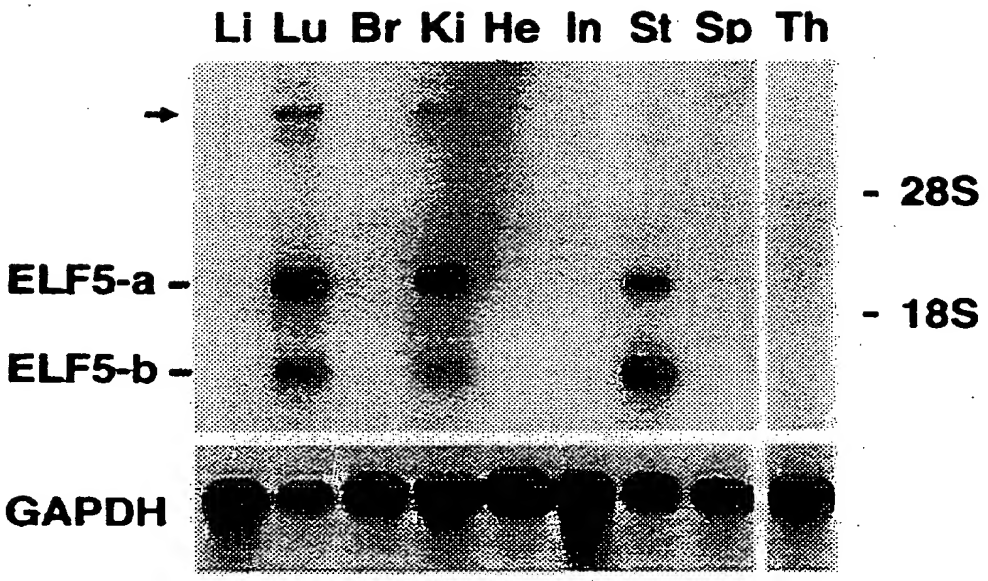


Figure 4b

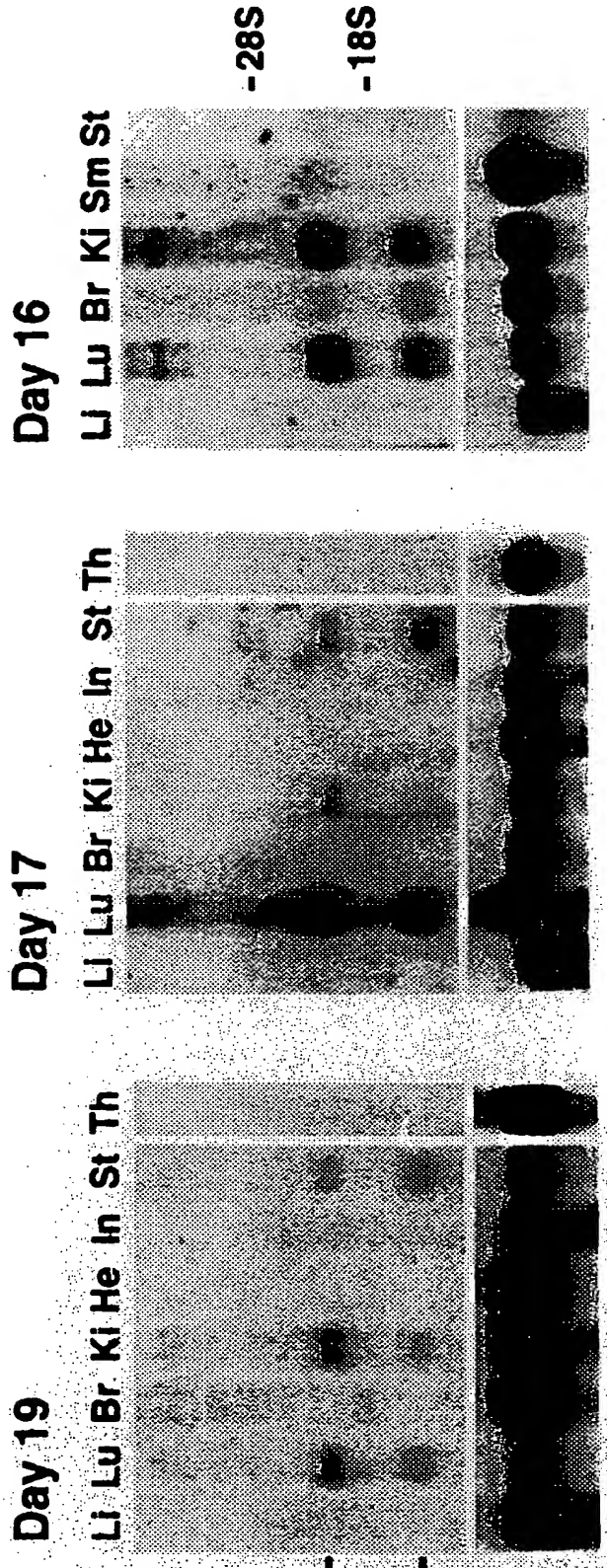

-28S
-18S
Day 16
Li Lu Br Ki Sm St
Day 17
Li Lu Br Ki He In St Th
Day 19
Li Lu Br Ki He In St Th
ELF5-a
ELF5-b
GAPDH

Figure 4c

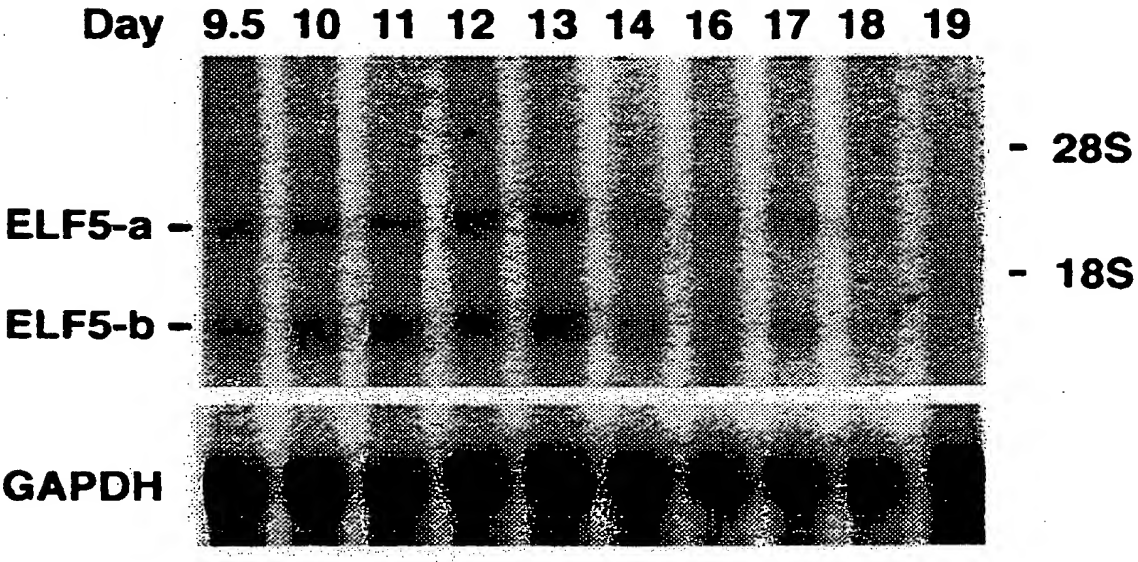


Figure 4d

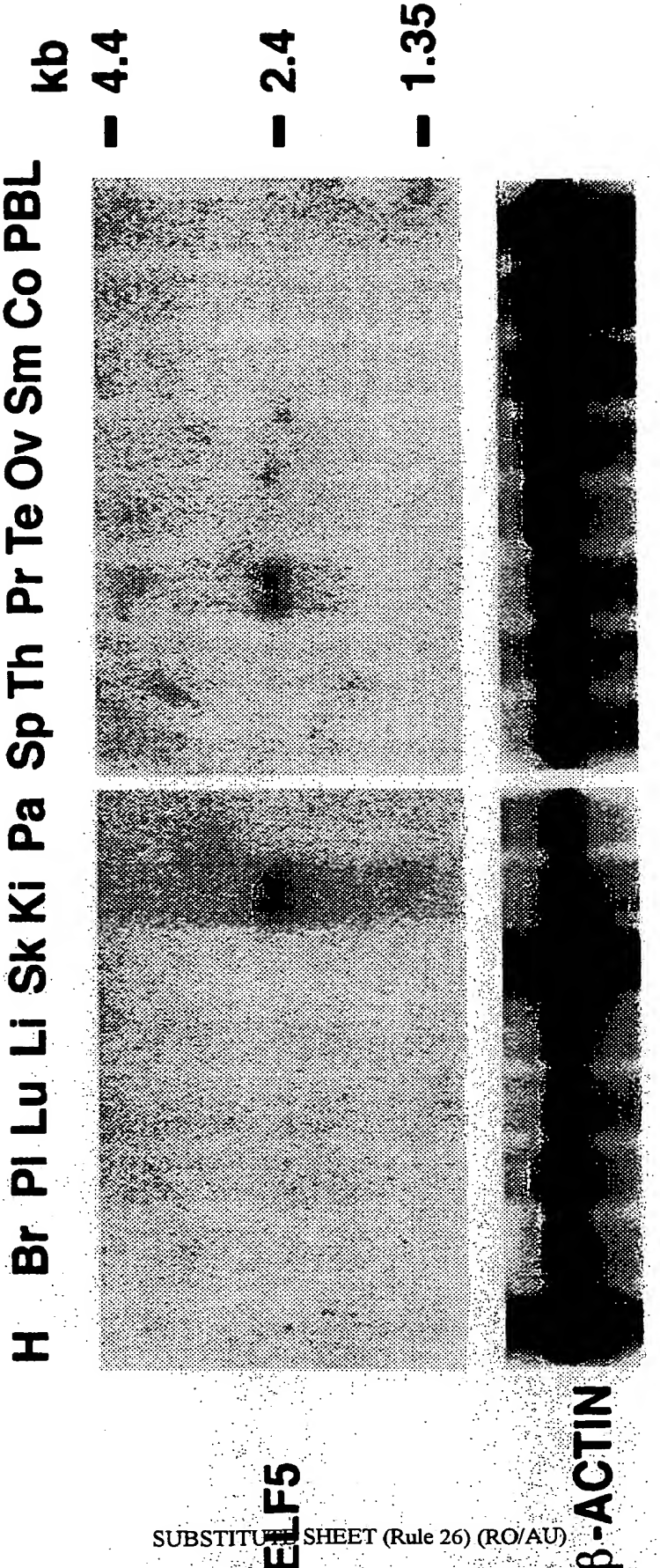


Figure 5a

T0ET80' EH09870

Figure 5b

PCT/AU99/00691 09/786043

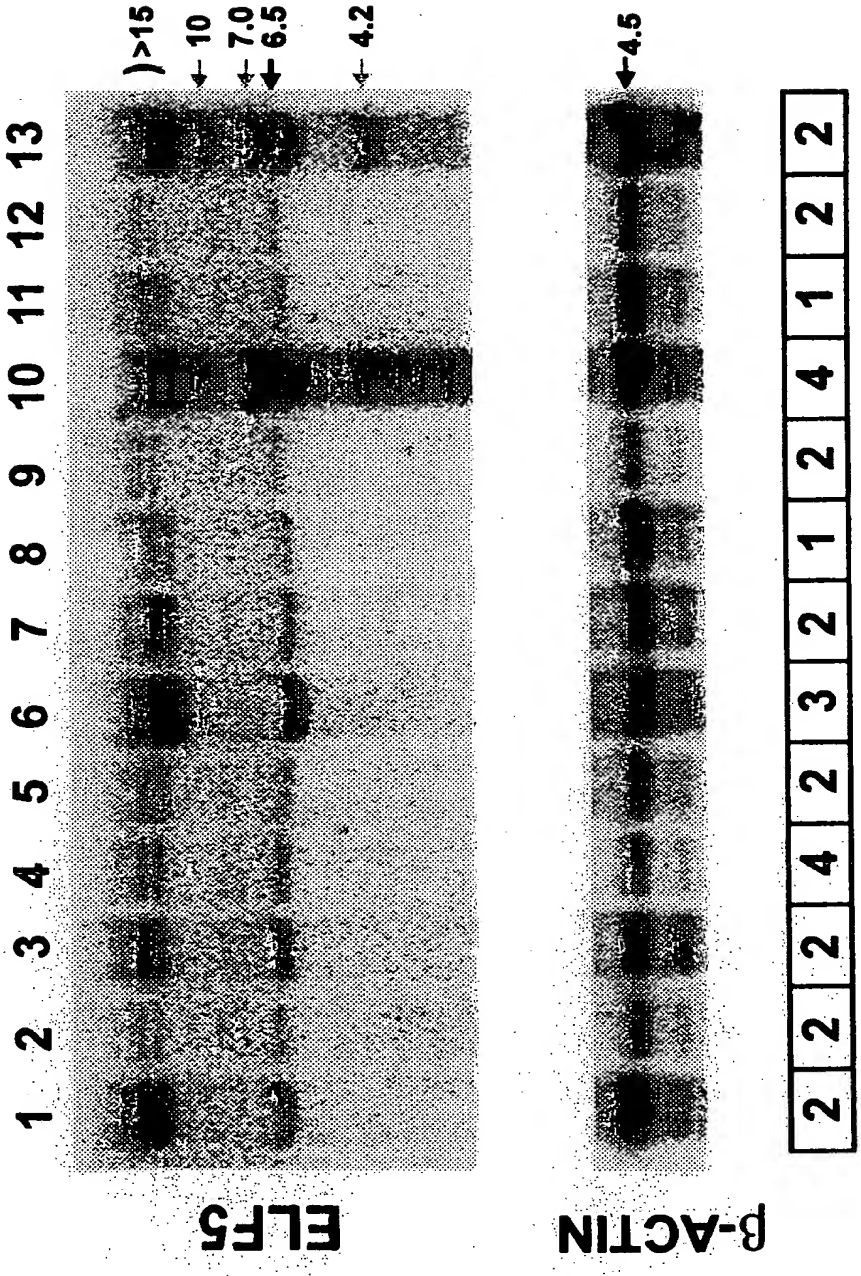
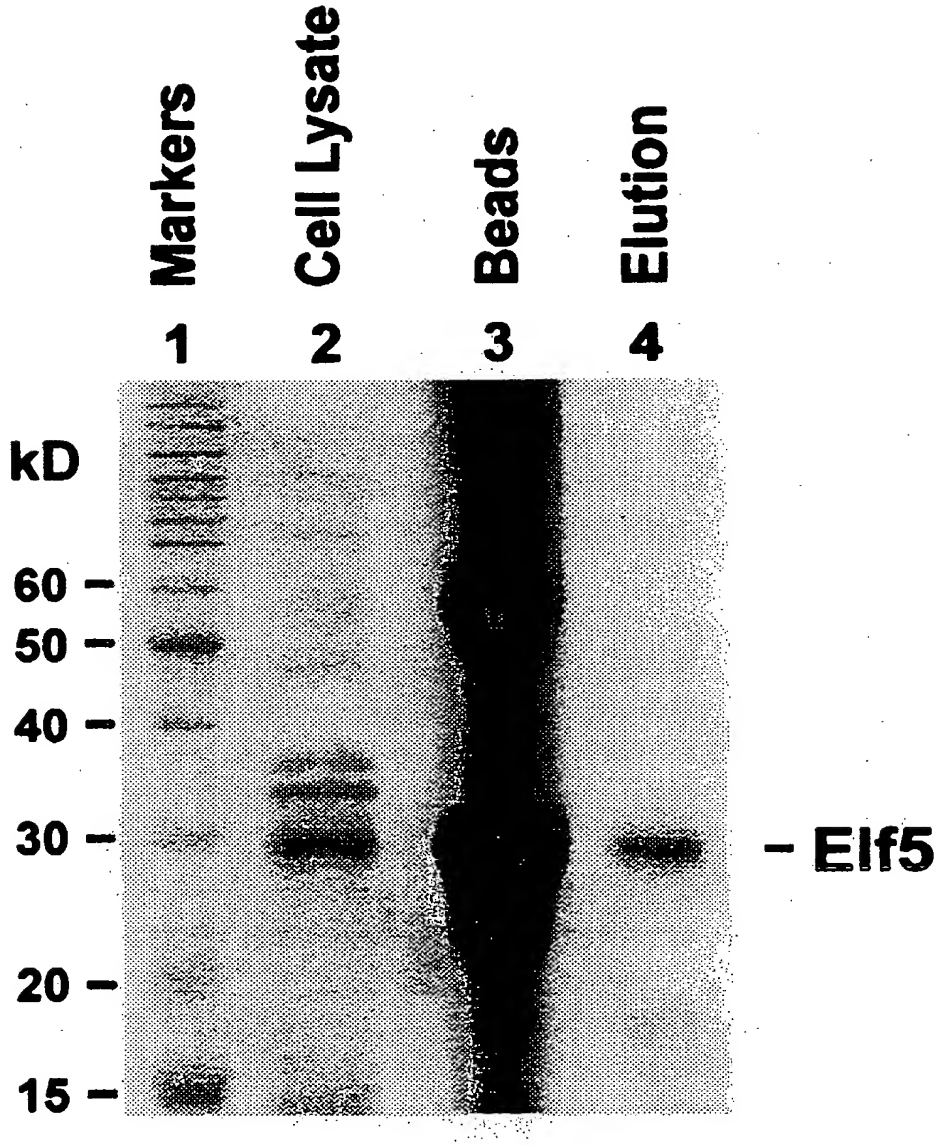

>15
10
7.0
6.5
4.2
4.5
1 2 3 4 5 6 7 8 9 10 11 12 13
2 2 2 4 2 3 2 1 2 4 1 2 2
ELF5
β-ACTIN

Figure 5c


Markers
Cell Lysate
Beads
Elution
1
2
3
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kD
60
50
40
30
20
15
Elf5

Figure 6a

TO2T80:E40880/90

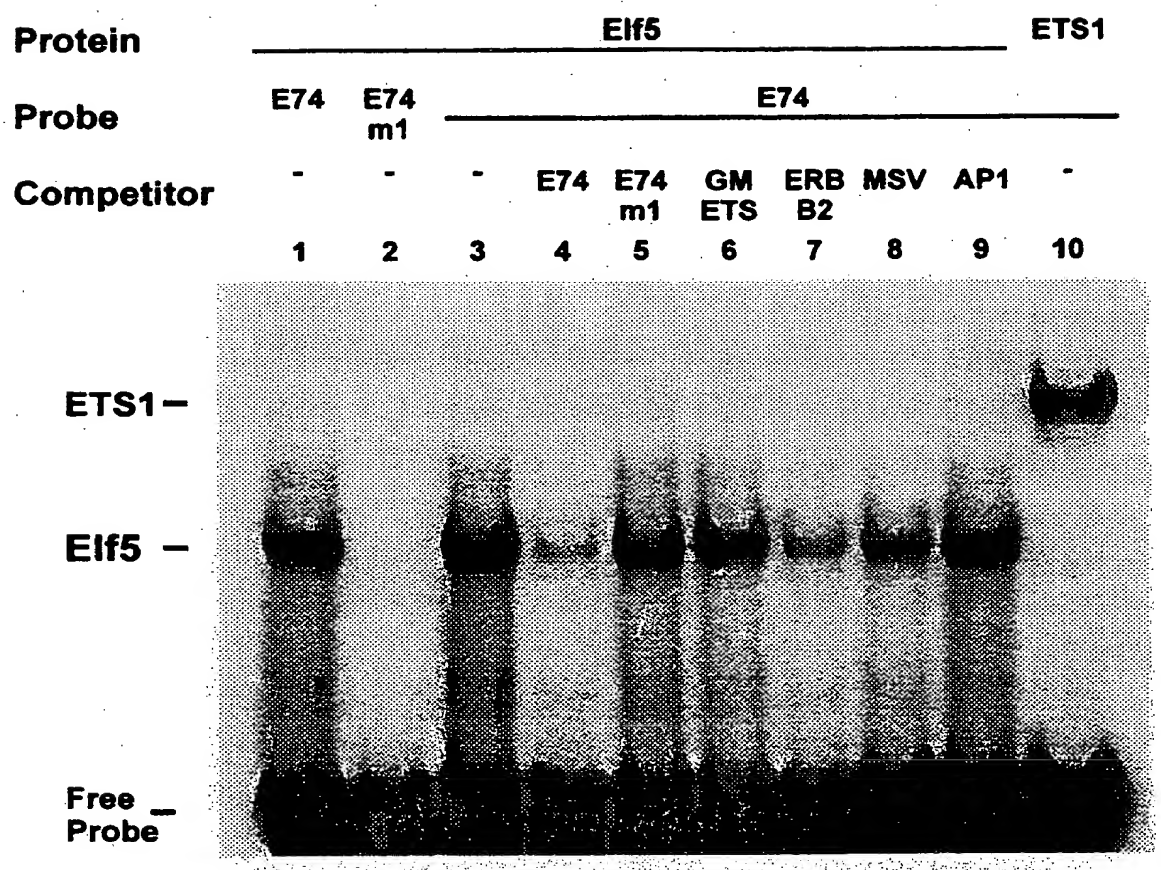
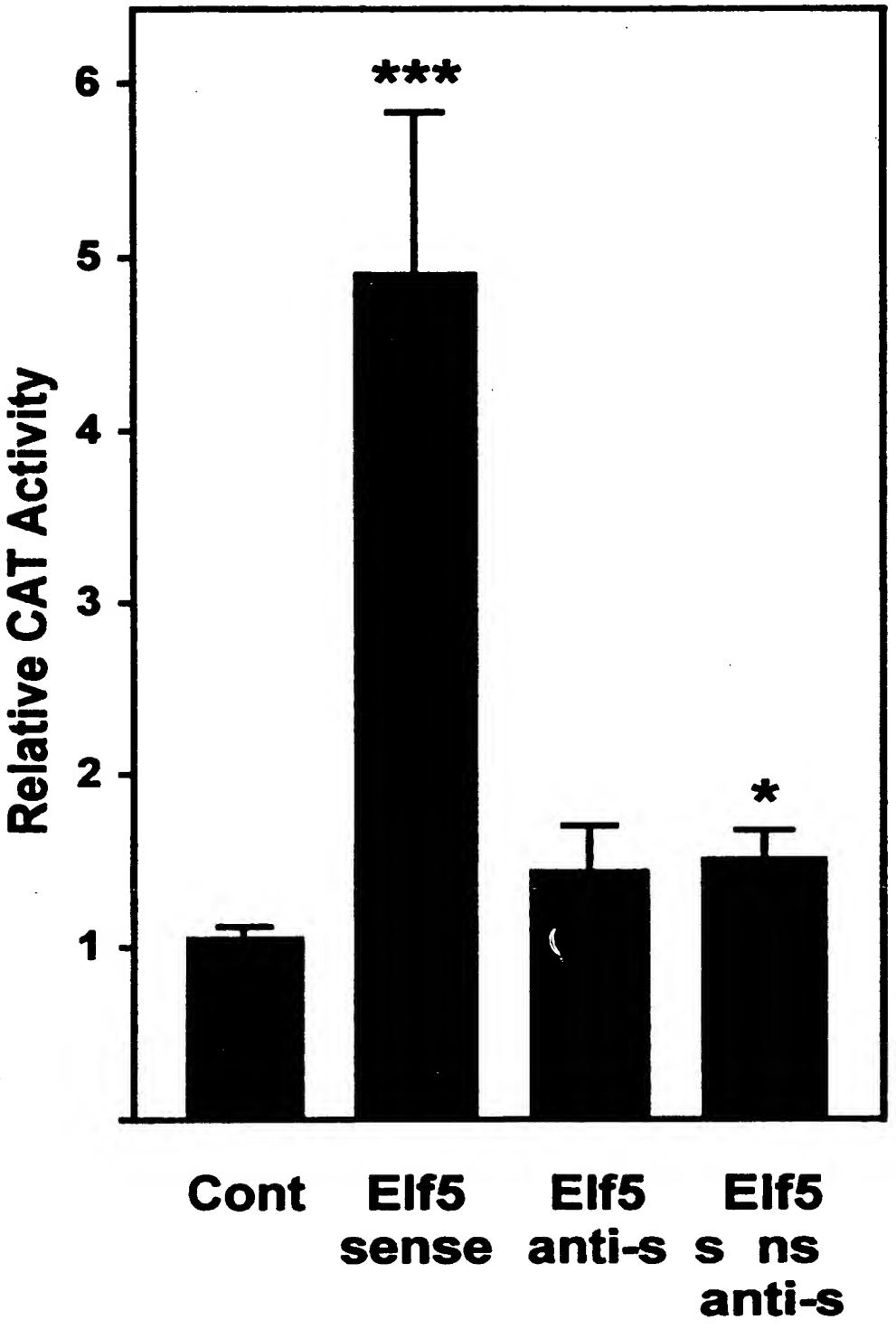


Figure 6b



PCT/AU99/00691 09.08.2000

Figure 7

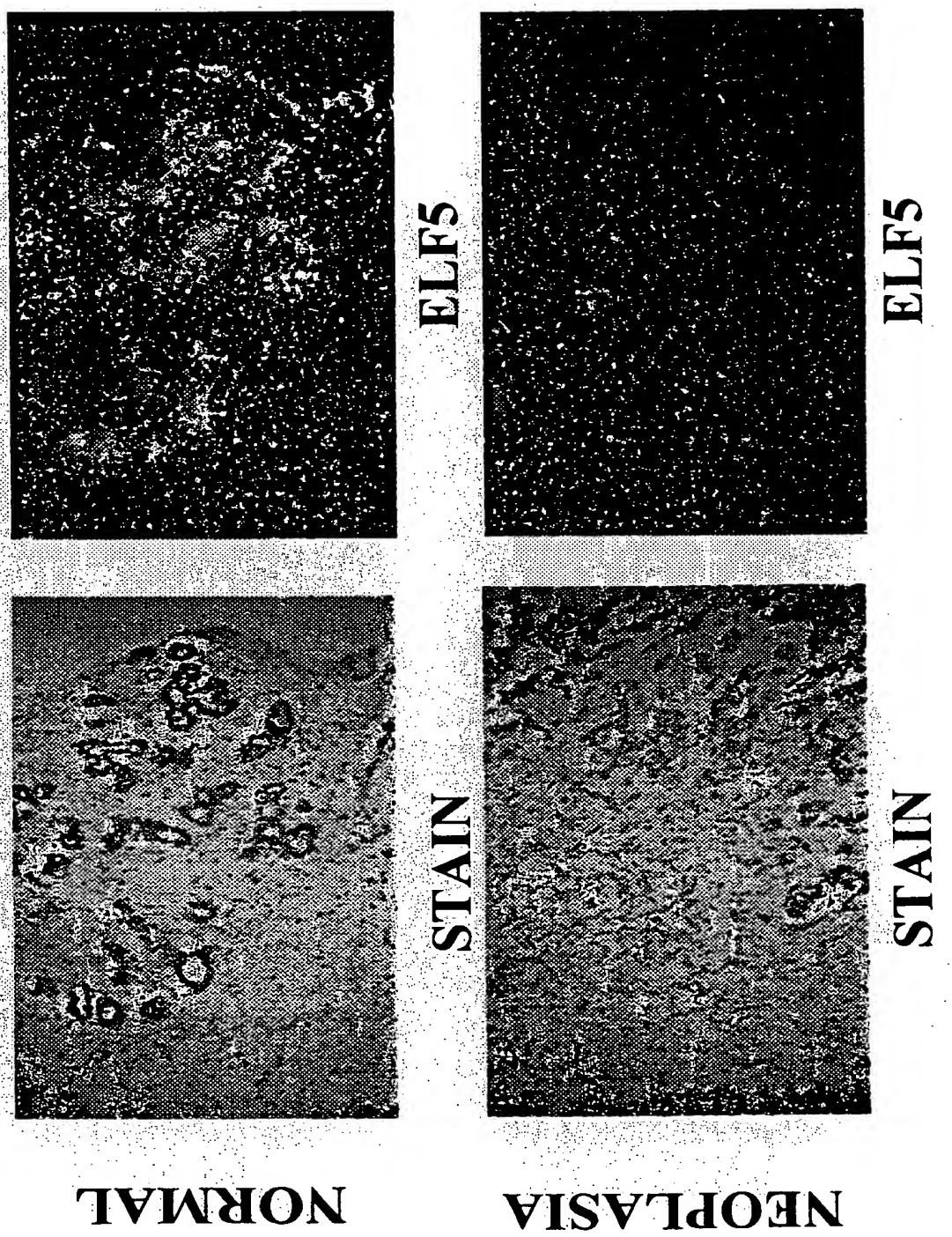


Figure 8